

Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

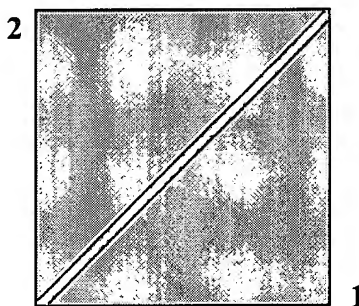
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

seq 2
seq 1

Sequence 1 lcl|seq_1 Length 411 (1 .. 411)

Sequence 2 lcl|seq_2 Length 411 (1 .. 411)


NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 790 bits (2041), Expect = 0.0
 Identities = 395/411 (96%), Positives = 407/411 (98%)

```

Query: 1  MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
          MAAPDLLDPKSAAQNSKPRLSFS+KPTVLASRVESD+ INVMKWKTVSTIFLVVLYLII
Sbjct: 1  MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60

Query: 61  GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120
          GA VFKALEQP EISQRTTIVIQKQTFI+QH+CVNSTELDELIQQIVAAINAGIIPLG+
Sbjct: 61  GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121  SNQISHWDLGSSFFFAAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
          SNQ+SHWDLGSSFFFAAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
Sbjct: 121  SNQVSHWDLGSSFFFAAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181  LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
          LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPA+IFKHIEGWSALD
Sbjct: 181  LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241  AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300
          AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS
Sbjct: 241  AIYFVVITLTTIGFGDYVAGGSDIEYLDIFYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301  KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360
          KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATS+KRKLSAELAGNHNQ
Sbjct: 301  KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

Query: 361  ELTPCRRTLNVNHLTNERDVLPLLLKTESIYLNGLTPHCAGEEIAVIENIK 411
          ELTPCRRTLNVNHLT+ER+VLPPLLK ESIYLNGLTPHCAGE+IAVIEN+K
Sbjct: 361  ELTPCRRTLNVNHLTSEREVLPLLLKAESIYLNGLTPHCAGEDIAVIENMK 411
  
```

CPU time: 0.04 user secs. 0.00 sys. secs 0.04 total secs.

Lambda	K	H
0.323	0.138	0.407

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1651

Number of Sequences: 0

Number of extensions: 121

Number of successful extensions: 3

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 411

length of database: 486,132,453

effective HSP length: 130

effective length of query: 281

effective length of database: 486,132,323

effective search space: 136603182763

effective search space used: 136603182763

T: 9

A: 40

X1: 16 (7.5 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (22.0 bits)

S2: 76 (33.9 bits)



Blast 2 Sequences results

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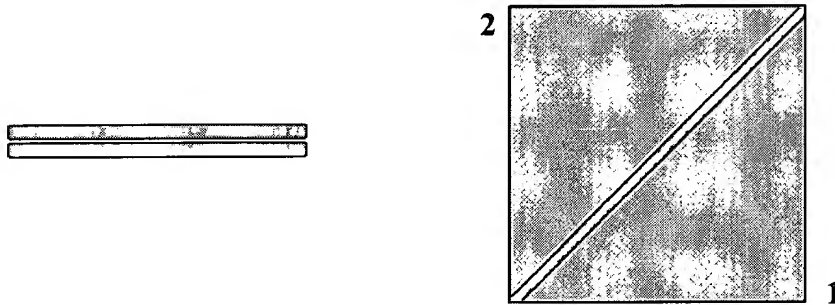
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align ☐

Sequence 1 lcl|seq_1 Length 411 (1 .. 411)

Sequence 2 lcl|seq_2 Length 411 (1 .. 411)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 810 bits (2092), Expect = 0.0
 Identities = 410/411 (99%), Positives = 410/411 (99%)

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKT VSTIFLVVVLVLII 60
 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKT VSTIFLVVVL LII
 Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKT VSTIFLVVLYLII 60

Query: 61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGI IPLGNT 120
 GATVFKALEQPHEISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGI IPLGNT
 Sbjct: 61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGI IPLGNT 120

Query: 121 SNQISHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
 SNQISHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
 Sbjct: 121 SNQISHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD
 Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVWFVILVGLAYFAAVLSMIGDWLRVIS 300
 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVWFVILVGLAYFAAVLSMIGDWLRVIS
 Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVWFVILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360
 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ
 Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRTL SVNHLTNERDVL PPLLKTESIYLNGLTPHCAGEEIAVIENIK 411
 ELTPCRRTL SVNHLTNERDVL PPLLKTESIYLNGLTPHCAGEEIAVIENIK
 Sbjct: 361 ELTPCRRTL SVNHLTNERDVL PPLLKTESIYLNGLTPHCAGEEIAVIENIK 411

← SAME AS
 INSTANT
 SEQ #D NO: 2

CPU time: 0.03 user secs. 0.00 sys. secs 0.03 total secs.

Lambda	K	H
0.323	0.139	0.411

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1683

Number of Sequences: 0

Number of extensions: 113

Number of successful extensions: 3

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 411

length of database: 486,132,453

effective HSP length: 130

effective length of query: 281

effective length of database: 486,132,323

effective search space: 136603182763

effective search space used: 136603182763

T: 9

A: 40

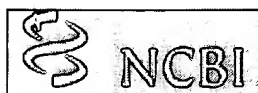
X1: 16 (7.5 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (22.0 bits)

S2: 76 (33.9 bits)



Blast 2 Sequences results

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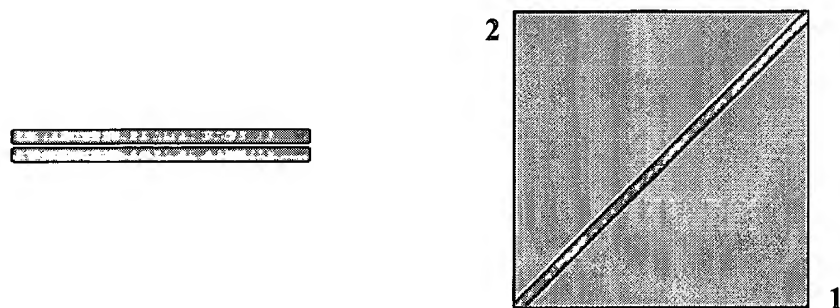
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.6 [Apr-09-2003]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.0** wordsize: **3** Filter ☐ Align

Sequence 1 lcl|seq_1 Length 411 (1 .. 411)

Sequence 2 lcl|seq_2 Length 411 (1 .. 411)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 807 bits (2084), Expect = 0.0
 Identities = 410/411 (99%), Positives = 410/411 (99%)

MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60
 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60

Query: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60
 Sbjct: 1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60

Query: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
 Sbjct: 61 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120

Query: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
 Sbjct: 121 SNQVSHWDLGSSFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180

Query: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
 Sbjct: 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Query: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300
 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300
 Sbjct: 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDWLRVIS 300

Query: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360
 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360
 Sbjct: 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360

Query: 361 ELTPCRRTLSVNHLTSEREVLPLLLKAESIYNGLTPHCAGEDIAVIENMK 411
 ELTPC RTLSVNHLTSEREVLPLLLKAESIYNGLTPHCAGEDIAVIENMK
 Sbjct: 361 ELTPCMRTLSVNHLTSEREVLPLLLKAESIYNGLTPHCAGEDIAVIENMK 411

SEQ 4
 AS INSTANT

CPU time: 0.01 user secs. 0.01 sys. secs 0.02 total secs.

Lambda	K	H
0.323	0.138	0.407

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1591

Number of Sequences: 0

Number of extensions: 119

Number of successful extensions: 3

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 411

length of database: 486,132,453

effective HSP length: 130

effective length of query: 281

effective length of database: 486,132,323

effective search space: 136603182763

effective search space used: 136603182763

T: 9

A: 40

X1: 16 (7.5 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (22.0 bits)

S2: 76 (33.9 bits)



Your request has been successfully submitted and put into the Blast Queue.

Query = (411 letters)

The request ID is

or

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi in

Number of: Descriptions Alignments

Alignment view

Format for PSI-BLAST ☐ with inclusion threshold:

Limit results by or select from:

Expect value range:



Your request has been successfully submitted and put into the Blast Queue.

SEQ 2 (NR)

Query = (411 letters)

The request ID is 1062182819-16887-878985.BLASTQ3

Format! or **Reset all**

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi in

Number of: Descriptions Alignments

Alignment view

Format for PSI-BLAST ☐ with inclusion threshold:

Limit results by or select from:

Expect value
range:



Your request has been successfully submitted and put into the Blast Queue.

SEQ (PAT)

Query = (411 letters)

The request ID is

or

The results are estimated to be ready in 0 seconds but may be done sooner.

Please press "FORMAT!" when you wish to check your results. You may change the formatting options for your result via the form below and press "FORMAT!" again. You may also request results of a different search by entering any other valid request ID to see other recent jobs.

Format

Show ☒ Graphical Overview ☒ Linkout ☒ Sequence Retrieval ☒ NCBI-gi in

Number of: Descriptions Alignments

Alignment view

Format for PSI-BLAST ☐ with inclusion threshold:

Limit results by or select from:

Expect value
range: